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1645

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## RAW SEQUENCE LISTING

DATE: 07/18/2001

PATENT APPLICATION: US/09/000,004A

TIME: 12:01:49

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Output Set: N:\CRF3\07182001\I000004A.raw

#15

CD

7/20/02

ENTERED

3 <110> APPLICANT: Tsilibary, Photini-Effie  
4 Charonis, Aristidis S.  
5 Setty, Suman  
6 Mauer, Michael  
8 <120> TITLE OF INVENTION: ANALYSIS OF ALPHA INTEGRINS FOR THE DIAGNOSIS OF DIABETIC  
NEPHROPATHY  
10 <130> FILE REFERENCE: 600.314USWO  
12 <140> CURRENT APPLICATION NUMBER: US 09/000,004A  
C--> 13 <141> CURRENT FILING DATE: 2001-06-19  
15 <150> PRIOR APPLICATION NUMBER: US 60/001,387  
16 <151> PRIOR FILING DATE: 1995-07-21  
18 <150> PRIOR APPLICATION NUMBER: US 60/001,861  
19 <151> PRIOR FILING DATE: 1995-08-03  
21 <150> PRIOR APPLICATION NUMBER: US 60/016,700  
22 <151> PRIOR FILING DATE: 1996-05-02  
24 <150> PRIOR APPLICATION NUMBER: PCT/US96/12067  
25 <151> PRIOR FILING DATE: 1996-07-19  
27 <160> NUMBER OF SEQ ID NOS: 16  
29 <170> SOFTWARE: PatentIn version 3.1  
31 <210> SEQ ID NO: 1  
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33 <212> TYPE: DNA  
34 <213> ORGANISM: Rattus  
36 <220> FEATURE:  
37 <221> NAME/KEY: CDS  
38 <222> LOCATION: (420)..(3959)  
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47 acacagcctg ggtagctgcc agtgagattt cagggacgga gcgcgcaaag gggggggaaa 180  
49 tgtggcaatc catctgggat gtgagacgcg tggagagggc ttagcagcat ttgaccaaaa 240  
51 cacaggaaat cactcctcca cagctcctgg gcgcagcagc ggctggggcc actgccggac 300  
53 accctcggag accacacgag tgaccacgag cgcaagtcgc cagcgtcccg gttctgcctg 360  
55 ttcttgccag ctcttgccca cgaaccggca cgtagctggt tccagcagcc gctccagca 419  
57 atg gtc ccc agg cgt cct gcc agc cta gag gtc act gta gcc tgc ata 467  
58 Met Val Pro Arg Arg Pro Ala Ser Leu Glu Val Thr Val Ala Cys Ile  
59 1 5 10 15  
61 tgg ctt ctc acg gtc atc cta ggc ttc tgc gtc tcc ttc aat gtt gat 515  
62 Trp Leu Leu Thr Val Ile Leu Gly Phe Cys Val Ser Phe Asn Val Asp  
63 20 25 30  
65 gtg aaa aac tca atg agt ttc agt ggc cca gta gag gac atg ttt gga 563  
66 Val Lys Asn Ser Met Ser Phe Ser Gly Pro Val Glu Asp Met Phe Gly  
67 35 40 45  
69 tac act gtt caa caa tat gaa aac gaa gaa ggc aaa tgg gtt ctt att 611  
70 Tyr Thr Val Gln Gln Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile  
71 50 55 60  
73 ggt tct cct tta gtt ggc caa ccc aaa gca aga act gga gat gtc tat 659

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77	aag	tgt	ccg	gtt	ggg	aga	gag	aga	gca	atg	cct	tgc	gtg	aag	ttg	gac	707
78	Lys	Cys	Pro	Val	Gly	Arg	Glu	Arg	Ala	Met	Pro	Cys	Val	Lys	Leu	Asp	
79					85					90					95		
81	ttg	cca	gtt	aac	aca	tcg	atc	ccc	aat	gtc	aca	gaa	ata	aag	gaa	aac	755
82	Leu	Pro	Val	Asn	Thr	Ser	Ile	Pro	Asn	Val	Thr	Glu	Ile	Lys	Glu	Asn	
83				100					105					110			
85	atg	aca	ttt	gga	tca	act	tta	gtc	acc	aac	ccg	aat	gga	gga	ttt	ctg	803
86	Met	Thr	Phe	Gly	Ser	Thr	Leu	Val	Thr	Asn	Pro	Asn	Gly	Gly	Phe	Leu	
87			115					120					125				
89	gca	tgt	ggg	ccc	ttg	tat	gcc	tat	aga	tgt	gga	cat	ttg	cat	tat	aca	851
90	Ala	Cys	Gly	Pro	Leu	Tyr	Ala	Tyr	Arg	Cys	Gly	His	Leu	His	Tyr	Thr	
91		130					135					140					
93	act	gga	ata	tgt	tct	gat	gtc	agt	cct	aca	ttt	caa	gtt	gtg	aac	tcc	899
94	Thr	Gly	Ile	Cys	Ser	Asp	Val	Ser	Pro	Thr	Phe	Gln	Val	Val	Asn	Ser	
95	145				150					155					160		
97	ttt	gcc	cct	gta	caa	gaa	tgc	agc	acc	cag	ctg	gac	ata	gtc	atc	gtc	947
98	Phe	Ala	Pro	Val	Gln	Glu	Cys	Ser	Thr	Gln	Leu	Asp	Ile	Val	Ile	Val	
99				165					170					175			
101	ctg	gat	ggc	tcc	aac	agc	atc	tac	ccc	tgg	gaa	agt	gtc	atc	gcc	ttt	995
102	Leu	Asp	Gly	Ser	Asn	Ser	Ile	Tyr	Pro	Trp	Glu	Ser	Val	Ile	Ala	Phe	
103				180					185					190			
105	tta	aac	gac	ctt	ctt	aag	agg	atg	gat	att	ggc	cct	aag	cag	aca	cag	1043
106	Leu	Asn	Asp	Leu	Leu	Lys	Arg	Met	Asp	Ile	Gly	Pro	Lys	Gln	Thr	Gln	
107			195					200					205				
109	gtc	ggg	att	gta	cag	tat	gga	gag	aat	gta	acc	cat	gag	ttc	aac	ctc	1091
110	Val	Gly	Ile	Val	Gln	Tyr	Gly	Glu	Asn	Val	Thr	His	Glu	Phe	Asn	Leu	
111		210				215						220					
113	aat	aag	tat	tca	tcc	aca	gaa	gag	gtc	ctt	gtc	gca	gca	aac	aaa	ata	1139
114	Asn	Lys	Tyr	Ser	Ser	Thr	Glu	Glu	Val	Leu	Val	Ala	Ala	Asn	Lys	Ile	
115	225				230					235					240		
117	ggc	cga	cag	gga	ggc	ctc	caa	acg	atg	aca	gcc	ctt	gga	ata	gac	aca	1187
118	Gly	Arg	Gln	Gly	Gly	Leu	Gln	Thr	Met	Thr	Ala	Leu	Gly	Ile	Asp	Thr	
119				245					250					255			
121	gcc	agg	aaa	gag	gca	ttc	act	gaa	gct	cgg	ggt	gcc	agg	agg	gga	gtt	1235
122	Ala	Arg	Lys	Glu	Ala	Phe	Thr	Glu	Ala	Arg	Gly	Ala	Arg	Arg	Gly	Val	
123				260					265					270			
125	aaa	aaa	gtc	atg	gtt	att	gtg	acc	gac	gga	gaa	tcg	cat	gac	aac	tat	1283
126	Lys	Lys	Val	Met	Val	Ile	Val	Thr	Asp	Gly	Glu	Ser	His	Asp	Asn	Tyr	
127			275					280					285				
129	cgc	ctg	aaa	cag	gtc	atc	caa	gac	tgc	gag	gac	gaa	aac	att	cag	cga	1331
130	Arg	Leu	Lys	Gln	Val	Ile	Gln	Asp	Cys	Glu	Asp	Glu	Asn	Ile	Gln	Arg	
131		290					295					300					
133	ttt	tcc	ata	gct	atc	ctt	ggc	cac	tat	aac	agg	ggg	aac	tta	agc	act	1379
134	Phe	Ser	Ile	Ala	Ile	Leu	Gly	His	Tyr	Asn	Arg	Gly	Asn	Leu	Ser	Thr	
135	305				310					315					320		
137	gaa	aaa	ttt	gtg	gag	gaa	ata	aaa	tcg	atc	gca	agc	gag	ccc	acg	gaa	1427
138	Glu	Lys	Phe	Val	Glu	Glu	Ile	Lys	Ser	Ile	Ala	Ser	Glu	Pro	Thr	Glu	

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142	Lys His Phe Phe Asn Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val						
143		340		345		350	
145	aaa gct ctg gga gaa agg ata ttc gct ttg gaa gcg aca gct gac cag						1523
146	Lys Ala Leu Gly Glu Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln						
147		355		360		365	
149	tca gca gct tca ttt gag atg gaa atg tct cag act ggc ttc agt gct						1571
150	Ser Ala Ala Ser Phe Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala						
151		370		375		380	
153	cac tac tcc cag gac tgg gtc atg ctt gga gcg gtg gga gcc tat gac						1619
154	His Tyr Ser Gln Asp Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp						
155	385		390		395	400	
157	tgg aac gga act gtg gtc atg cag aag gct aac cag atg gtc atc cct						1667
158	Trp Asn Gly Thr Val Val Met Gln Lys Ala Asn Gln Met Val Ile Pro						
159		405		410		415	
161	cat aac acc acc ttt caa act gag ccc gcc aag atg aac gag cct ctg						1715
162	His Asn Thr Thr Phe Gln Thr Glu Pro Ala Lys Met Asn Glu Pro Leu						
163		420		425		430	
165	gct tct tat tta ggt tac aca gtg aac tcg gcc acc atc cct gga gat						1763
166	Ala Ser Tyr Leu Gly Tyr Thr Val Asn Ser Ala Thr Ile Pro Gly Asp						
167		435		440		445	
169	gtg ctc tac atc gct ggg cag cct cgg tac aat cat acg ggc cag gtc						1811
170	Val Leu Tyr Ile Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln Val						
171		450		455		460	
173	gtc atc tac aag atg gag gat ggg aac atc aac att ctg cag aca ctc						1859
174	Val Ile Tyr Lys Met Glu Asp Gly Asn Ile Asn Ile Leu Gln Thr Leu						
175	465		470		475	480	
177	ggc gga gag cag att ggt tcc tac ttt ggt agt gtc tta aca aca att						1907
178	Gly Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Thr Thr Ile						
179		485		490		495	
181	gac atc gac aaa gat tct tat act gat ctg ctt ctc gtc ggg gcc ccc						1955
182	Asp Ile Asp Lys Asp Ser Tyr Thr Asp Leu Leu Leu Val Gly Ala Pro						
183		500		505		510	
185	atg tac atg ggg aca gag aaa gag gaa cag ggc aag gtg tac gtg tac						2003
186	Met Tyr Met Gly Thr Glu Lys Glu Glu Gln Gly Lys Val Tyr Val Tyr						
187		515		520		525	
189	gct gtg aat cag aca agg ttt gaa tat caa atg agc ctg gaa cca att						2051
190	Ala Val Asn Gln Thr Arg Phe Glu Tyr Gln Met Ser Leu Glu Pro Ile						
191		530		535		540	
193	agg cag acc tgc tgc tca tcc ctg aag gat aat tca tgc acg aaa gaa						2099
194	Arg Gln Thr Cys Cys Ser Ser Leu Lys Asp Asn Ser Cys Thr Lys Glu						
195	545		550		555	560	
197	aac aag aat gag ccc tgc ggg gcc cgc ttc gga aca gca att gct gct						2147
198	Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala Ala						
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201	gta aaa gac ctc aac gtg gat gga ttt aat gac gtc gtg att gga gct						2195
202	Val Lys Asp Leu Asn Val Asp Gly Phe Asn Asp Val Val Ile Gly Ala						
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206	Pro	Leu	Glu	Asp	Asp	His	Ala	Gly	Ala	Val	Tyr	Ile	Tyr	His	Gly	Ser	
207			595					600					605				
209	ggc	aag	acc	ata	agg	gag	gcg	tat	gca	caa	cgc	att	cca	tca	ggt	ggg	2291
210	Gly	Lys	Thr	Ile	Arg	Glu	Ala	Tyr	Ala	Gln	Arg	Ile	Pro	Ser	Gly	Gly	
211			610					615					620				
213	gat	ggc	aag	acc	ctg	aaa	ttt	ttc	ggc	cag	tct	atc	cac	gga	gag	atg	2339
214	Asp	Gly	Lys	Thr	Leu	Lys	Phe	Phe	Gly	Gln	Ser	Ile	His	Gly	Glu	Met	
215	625						630					635				640	
217	gat	tta	aat	ggt	gac	ggt	ctg	act	gac	gtg	acc	att	gga	ggc	ctt	ggt	2387
218	Asp	Leu	Asn	Gly	Asp	Gly	Leu	Thr	Asp	Val	Thr	Ile	Gly	Gly	Leu	Gly	
219						645					650					655	
221	gga	gca	gcc	ctc	ttc	tgg	gcc	aga	gat	gtg	gct	gta	gtt	aaa	gtg	acc	2435
222	Gly	Ala	Ala	Leu	Phe	Trp	Ala	Arg	Asp	Val	Ala	Val	Val	Lys	Val	Thr	
223					660					665				670			
225	atg	aat	ttt	gaa	ccc	aat	aaa	gtg	aat	att	caa	aag	aaa	aac	tgc	cgt	2483
226	Met	Asn	Phe	Glu	Pro	Asn	Lys	Val	Asn	Ile	Gln	Lys	Lys	Asn	Cys	Arg	
227			675					680					685				
229	gtg	gag	ggc	aaa	gaa	aca	gtg	tgc	ata	aat	gct	aca	atg	tgt	ttt	cat	2531
230	Val	Glu	Gly	Lys	Glu	Thr	Val	Cys	Ile	Asn	Ala	Thr	Met	Cys	Phe	His	
231			690					695					700				
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234	Val	Lys	Leu	Lys	Ser	Lys	Glu	Asp	Ser	Ile	Tyr	Glu	Ala	Asp	Leu	Gln	
235	705					710					715				720		
237	tac	cgt	gtc	acc	ctt	gat	tca	ctg	agg	cag	ata	tca	cgg	agc	ttt	ttt	2627
238	Tyr	Arg	Val	Thr	Leu	Asp	Ser	Leu	Arg	Gln	Ile	Ser	Arg	Ser	Phe	Phe	
239					725					730					735		
241	tct	gga	act	cag	gaa	agg	aag	att	caa	aga	aat	atc	acc	gtt	cga	gaa	2675
242	Ser	Gly	Thr	Gln	Glu	Arg	Lys	Ile	Gln	Arg	Asn	Ile	Thr	Val	Arg	Glu	
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245	tca	gaa	tgc	atc	agg	cac	tcc	ttc	tac	atg	ttg	gac	aaa	cat	gac	ttt	2723
246	Ser	Glu	Cys	Ile	Arg	His	Ser	Phe	Tyr	Met	Leu	Asp	Lys	His	Asp	Phe	
247			755					760					765				
249	cag	gac	tct	gtg	aga	gtg	act	ctg	gat	ttt	aat	ctc	act	gat	cca	gaa	2771
250	Gln	Asp	Ser	Val	Arg	Val	Thr	Leu	Asp	Phe	Asn	Leu	Thr	Asp	Pro	Glu	
251			770				775						780				
253	aat	ggt	cct	gta	ctt	gat	gac	gct	ctg	cca	aac	tca	gtc	cac	gaa	cac	2819
254	Asn	Gly	Pro	Val	Leu	Asp	Asp	Ala	Leu	Pro	Asn	Ser	Val	His	Glu	His	
255	785					790					795				800		
257	att	ccc	ttt	gcc	aaa	gac	tgt	gga	aac	aag	gaa	aga	tgc	att	tca	gac	2867
258	Ile	Pro	Phe	Ala	Lys	Asp	Cys	Gly	Asn	Lys	Glu	Arg	Cys	Ile	Ser	Asp	
259					805					810					815		
261	ctc	act	ctg	aat	gtg	tcc	acc	aca	gaa	aag	agc	ctg	ctg	atc	gtc	aag	2915
262	Leu	Thr	Leu	Asn	Val	Ser	Thr	Thr	Glu	Lys	Ser	Leu	Leu	Ile	Val	Lys	
263					820					825					830		
265	tcc	cag	cat	gac	aag	ttc	aac	gtt	agc	ctc	acc	gtc	aaa	aac	aaa	gga	2963
266	Ser	Gln	His	Asp	Lys	Phe	Asn	Val	Ser	Leu	Thr	Val	Lys	Asn	Lys	Gly	
267			835					840					845				
269	gac	agt	gcg	tac	aac	acc	agg	aca	gtg	gtg	cag	cat	tca	cca	aat	ctg	3011

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274 Ile Phe Ser Gly Ile Glu Glu Ile Gln Lys Asp Ser Cys Glu Ser Asn
275 865                      870                      875                      880
277 caa aat atc act tgc aga gtt gga tat cct ttc cta aga gca gga gaa      3107
278 Gln Asn Ile Thr Cys Arg Val Gly Tyr Pro Phe Leu Arg Ala Gly Glu
279                      885                      890                      895
281 acg gtt acc ttc aaa ata ata ttc cag ttt aac aca tcc cat ctc tcg      3155
282 Thr Val Thr Phe Lys Ile Ile Phe Gln Phe Asn Thr Ser His Leu Ser
283                      900                      905                      910
285 gaa aat gca atc att cac tta agt gca aca agt gac agt gag gag ccc      3203
286 Glu Asn Ala Ile Ile His Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro
287                      915                      920                      925
289 ctg gaa tct ctt aat gat aat gaa gta aat att tcc atc cca gta aaa      3251
290 Leu Glu Ser Leu Asn Asp Asn Glu Val Asn Ile Ser Ile Pro Val Lys
291                      930                      935                      940
293 tat gaa gtt gga ctg cag ttt tac agt tct gcg agt gaa cat cac att      3299
294 Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala Ser Glu His His Ile
295 945                      950                      955                      960
297 tca gtc gct gcc aat gag acg atc cct gag ttt att aac tcc act gag      3347
298 Ser Val Ala Ala Asn Glu Thr Ile Pro Glu Phe Ile Asn Ser Thr Glu
299                      965                      970                      975
301 gac att ggg aat gaa att aat gtc ttc tat acg att aga aag agg ggg      3395
302 Asp Ile Gly Asn Glu Ile Asn Val Phe Tyr Thr Ile Arg Lys Arg Gly
303                      980                      985                      990
305 cat ttc cca atg cca gaa ctt cag ctg tca att tca ttc ccc aat ttg      3443
306 His Phe Pro Met Pro Glu Leu Gln Leu Ser Ile Ser Phe Pro Asn Leu
307                      995                      1000                      1005
309 acg gca gat ggt tat cct gta ctg tac cca att gga tgg tca tct      3488
310 Thr Ala Asp Gly Tyr Pro Val Leu Tyr Pro Ile Gly Trp Ser Ser
311                      1010                      1015                      1020
313 tca gat aat gtg aac tgt aga ccc cgg agc ctt gag gac ccc ttt      3533
314 Ser Asp Asn Val Asn Cys Arg Pro Arg Ser Leu Glu Asp Pro Phe
315                      1025                      1030                      1035
317 ggc atc aac tct ggg aag aaa atg aca ata tcg aag tct gag gtt      3578
318 Gly Ile Asn Ser Gly Lys Lys Met Thr Ile Ser Lys Ser Glu Val
319                      1040                      1045                      1050
321 ctc aaa aga ggc aca atc cag gac tgc agt agt acg tgt gga gtt      3623
322 Leu Lys Arg Gly Thr Ile Gln Asp Cys Ser Ser Thr Cys Gly Val
323                      1055                      1060                      1065
325 gcc acc atc acg tgt agc ctc ctt cct tcc gac ctg agt caa gtg      3668
326 Ala Thr Ile Thr Cys Ser Leu Leu Pro Ser Asp Leu Ser Gln Val
327                      1070                      1075                      1080
329 aat gtc tcg ctc ctc ctg tgg aaa ccg act ttc ata aga gca cat      3713
330 Asn Val Ser Leu Leu Leu Trp Lys Pro Thr Phe Ile Arg Ala His
331                      1085                      1090                      1095
333 ttt tcc agc tta aac ctt act cta aga gga gaa ctt aag agt gaa      3758
334 Phe Ser Ser Leu Asn Leu Thr Leu Arg Gly Glu Leu Lys Ser Glu

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VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date